SEQUENCE LISTING

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<211> 2512
<212> DNA
<213> Mus musculus

<400> 1
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acaaaaggct ggtttcttga acatgcgttc cagtcccgtg acatgtgaac acataggttc 2460
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<210> 2
<211> 764
<212> PRT
<213> Mus musculus

<400> 2

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Gln Glu Asp Asp Phe Arg Val Thr Cys Lys Glu Leu His Arg Ile Pro
        35                  40                  45
Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu
    50                  55                  60
Lys Thr Ile Pro Ser Leu Ala Phe Ser Ser Leu Pro Asn Ile Ser Arg
65                  70                  75                  80
Ile Tyr Leu Ser Ile Asp Ala Thr Leu Gln Arg Leu Glu Pro His Ser
                85                  90                  95
Phe Tyr Asn Leu Ser Lys Met Thr His Ile Glu Ile Arg Asn Thr Arg
                100                 105                 110
Ser Leu Thr Tyr Ile Asp Pro Asp Ala Leu Thr Glu Leu Pro Leu Leu
        115                 120                 125
Lys Phe Leu Gly Ile Phe Asn Thr Gly Leu Arg Ile Phe Pro Asp Leu
    130                 135                 140
Thr Lys Ile Tyr Ser Thr Asp Ile Phe Phe Ile Leu Glu Ile Thr Asp
145                 150                 155                 160
Asn Pro Tyr Met Thr Ser Val Pro Glu Asn Ala Phe Gln Gly Leu Cys
                165                 170                 175
Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val
                180                 185                 190
Gln Gly His Ala Phe Asn Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn
        195                 200                 205
Lys Asn Lys Tyr Leu Thr Ala Ile Asp Asn Asp Ala Phe Gly Gly Val
    210                 215                 220
Tyr Ser Gly Pro Thr Leu Leu Asp Val Ser Ser Thr Ser Val Thr Ala
225                 230                 235                 240
Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Lys Asp
                245                 250                 255
Thr Trp Thr Leu Lys Lys Leu Pro Leu Ser Leu Ser Phe Leu His Leu
            260                 265                 270
Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn
        275                 280                 285
Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser
        290                 295                 300
Ser Ile Arg Asn Leu Arg Gln Arg Lys Ser Val Asn Ile Leu Arg Gly
305                 310                 315                 320
Pro Ile Tyr Gln Glu Tyr Glu Glu Asp Pro Gly Asp Asn Ser Val Gly
                325                 330                 335
Tyr Lys Gln Asn Ser Lys Phe Gln Glu Ser Pro Ser Asn Ser His Tyr
            340                 345                 350
Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Val Val Gly Phe Gly Gln
        355                 360                 365
Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Glu Ser His
    370                 375                 380
Tyr Asp Tyr Thr Val Cys Gly Asp Asn Glu Asp Met Val Cys Thr Pro
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2

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385                     390                     395                     400
Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Arg Phe
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            420                 425                 430
Ile Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Thr Val
            435                 440                 445
Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly
    450                 455                 460
Val Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu
465                 470                 475                 480
Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr
                485                 490                 495
Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu
            500                 505                 510
Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Arg
            515                 520                 525
Leu Asp Arg Lys Ile Arg Leu Arg His Ala Tyr Thr Ile Met Ala Gly
    530                 535                 540
Gly Trp Val Ser Cys Phe Leu Leu Ala Leu Leu Pro Met Val Gly Ile
545                 550                 555                 560
Ser Ser Tyr Ala Lys Val Ser Ile Cys Leu Pro Met Asp Thr Asp Thr
                565                 570                 575
Pro Leu Ala Leu Ala Tyr Ile Val Leu Val Leu Leu Leu Asn Val Val
            580                 585                 590
Ala Phe Val Val Val Cys Ser Cys Tyr Val Lys Ile Tyr Ile Thr Val
            595                 600                 605
Arg Asn Pro Gln Tyr Asn Pro Arg Asp Lys Asp Thr Lys Ile Ala Lys
    610                 615                 620
Arg Met Ala Val Leu Ile Phe Thr Asp Phe Met Cys Met Ala Pro Ile
625                 630                 635                 640
Ser Phe Tyr Ala Leu Ser Ala Leu Met Asn Lys Pro Leu Ile Thr Val
                645                 650                 655
Thr Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Leu Asn Ser Cys
                660                 665                 670
Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp
            675                 680                 685
Val Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln
    690                 695                 700
Ala Tyr Gln Gly Gln Arg Val Cys Pro Asn Asn Ser Thr Gly Ile Gln
705                 710                 715                 720
Ile Gln Lys Ile Pro Gln Asp Thr Arg Gln Ser Leu Pro Asn Met Gln
                725                 730                 735
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            740                 745                 750
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<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

<400> 3
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gcagggcact gagaatgtgg cgacagcgcg caacgatgaa gtagcccaga gggtcccttg  180
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gaaaatgagg ccagggtccc                                             200
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<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

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tcgtggtgtg tgttggggtg tgcgcggata tctggtcagt ccctgtacaa attcaatccc 180
ccatgctcgg gaaggtcagc                                            200
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